

		10	20	30	40	50	60	70	80	90	100
p38	MSQERPTFYRQELNKTINEVPERYQNLSPVGSAGYGVCAAFDTKTGRVAVVKLSAPFQSIHAKRTYRELRLKKHKKHENVIGLLDOVFTPARSLEEFN										
ikk	MSMSPSLPTQTGCA--WENKER-----LGTGGFGNVIRAHNQVIGEQIAIKQCQDEL-SPKNDRQMCLEIQIHRRLNHPNVVAAARDVPEGHQLAPND										
Consensus	.wqerPslprQecna..WENKER.....LGsGa%GnVcaah#qkTgerlA!Kqcrrel.SiInadRtcrE!r!\$rr\$HnHnV!aarDVfegarnLaen#										
		110	120	130	140	150	160	170	180	190	200
p38	---DYYLVTHLMGADL-----NNIVKCCQLTDDHVQFLIYQILRGLKYTHSADIHROLKPSNLAVNEDCEL---KILDFGLARHTDDEN--TGVATRWYRA										
ikk	LPLLAMEYCCGGDLRRYLNOFENCGLREGAILTLSDIASALRYLHENRIIHROLKPENIVLQQGEKRLIHKIIDLGYAKELDQGSCLTSFVGTLLQYLA										
Consensus	.dllanehcqGaDL...N#IenCcglr#da!qfL!s#IaraLrY!HearI!HROLKPeNial#dcer...KIIDLGLareld#en..!gxVatrqYra										
		210	220	230	240	250	260	270	280	290	300
p38	PEITMLNMHYNOTVDIMSVCIMARELLIG-RTLFPGIOHID-----QLKLILRLVGTFGRELLKKISSESA-RNYIQSLAQMPKHNMFANVFIGANPLAYD										
ikk	PEL-LEQKQYTVVDYNSFGYLAFECITIGEPFLPNMQPVQNMHSKVRQKSEVDIVYSEDINGIVKFSSESPFPNNINSLVLAERLEKHLQLMLTHQPRQRG										
Consensus	PEI.L#qqhYngIVDIMSfgciaaEcitIG.Rp1lPnt#h!#.....rqKlelrivgseda#glkKISSESa.rNni!\$Slaaerlenfa#lniga#Prard										
		310	320	330	340	350	360	370	380	390	
p38	---LLEK-----MLVLOSOKRITTAQAL--AHAYFAQYHDPDDEPVADPYDQSFESROLLIDENKSLTYDEVISFVPPPLDQEEMES										
ikk	VDPQYGPNGCFRALDDILNLKLVHILNMVTGTHITYPVMEDESLSQSLKTRIREDTGILETDQELLQEAQLVLLPKPATQCISDSKTNMEG										
Consensus	ldeq.....nralDddlr!kaaqal...ahat!aqYhdm#DEpladlkdr!rEdrdiled#qellqaell!llpdkPadQcen#S.....										

Fig. 1(a)

1	10	20	30	40	50	60	70	80	90	100
p38										
MEK-1										
Consensus										
	MPKKKPTPIQLNPAPDGSAYNGTSSAETNLERLQKKLEELDEQQRKRLERFLTQKQGVGELKODDQEKJSELGAGNGGVVFKVSKKSPGSLVMARKLIIH	MSQERPTFYRQELNKTITHEVPERYQNLSPVSGGAYGSVCARFOTKTKGHRVAVYKKLS								
qqqrleazrqqlKktgeekdrX%#jlselGagagaycaefdkksgshrwarkKLIh									
101	110	120	130	140	150	160	170	180	190	200
p38										
MEK-1										
Consensus										
	RFQSIITHAKRTVRELRLKKHKNHNVIGLLDVFPTARSLEEFNDVYLYTHLNGADLNINIVK-CQKLTDHVVQFLIYQILRLGLKYIHSAO-IITHROLKPS									
	LEIKPAIR-NQIITRELQVLHECNPSYIVGVFGAFYSOGEIS-----ICMEHHDGGSLDQVLKAGRIPEQILGKVSIAVYKGLTYLREKHKIMHRDVKPS									
	relqpaIr..nrIIRRELRLHhecnhen!Gllldetpareie.....icneh\$dgadL#lLK.eqrIp##hlqkllleIr-GLkyIread.IIHRDLKPS									
201	210	220	230	240	250	260	270	280	290	300
p38										
MEK-1										
Consensus										
	NLAVNEDCELKXLDGLARHYDODENTG-YVATRNRYRAPEIMLNMHYNTQYDIMSVCIMARELLTGRTLFFPGTDHIOQKLILRLVGTGPAELLKKKISSE									
	NILVNSRGEIKLDFGVSGQLDISHANSFVGTSGYMSPE-RLQGTHYSVQSDIASMGLSIVENAVRGYPIPPPOAKLELLFGCQVEGDRAETPPRPRTF									
	NlaVNERcEiKicDFGlarqldDehen.XVaItrayr.eP.e.rL%gnHYNqqsDIASngcIsaEetGRTLIIPeDol#qellIgrqVegdehEllkrIrs									
301	310	320	330	340	350	360	370	380	390	400
p38										
MEK-1										
Consensus										
	SARNYIQSLAQMPKHN-FANVFIGNAPLAVOLLEKMLVDSOKRITTAQALAHAYFAQYHDPDDEPVADPYDQGSFESROLLIDEMKSLTYDVEISFYVPP									
	GRPLSYGMDSRPHAFIFELLOVYNPPPKLPSSGVFSLEFDQFNKCLIKNPAERADLK-----QLMVHRAIKKSDRAEEYDFAGMLCSITGLNQKPSPTH									
	garnsiqsgaqrPkha.FanlddigeNelapdllegnlsL#fdr!naeqalahaRerA#lh....#lnadaXqdr-f#ar#ldiaeeHlclIIdenqpfTPp									
401	408									
p38										
MEK-1										
Consensus										
	LDQEEMES									
	AASI									
	aaqa....									

Fig. 1(b)

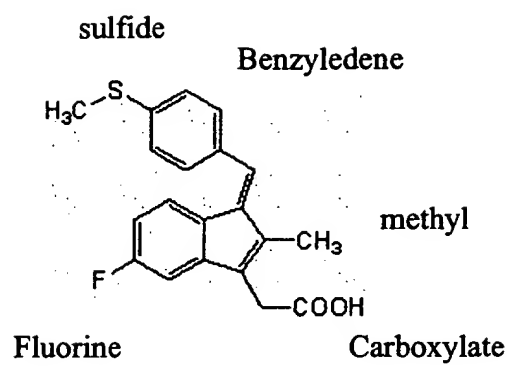


Fig. 2(a)

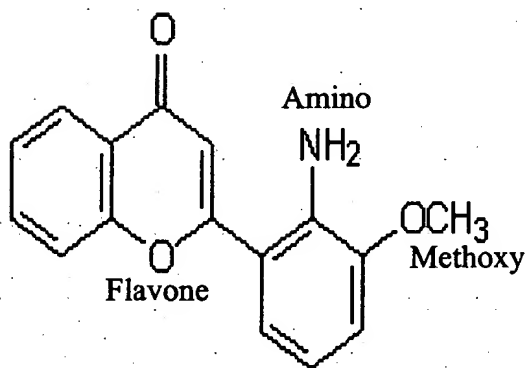


Fig. 2(b)

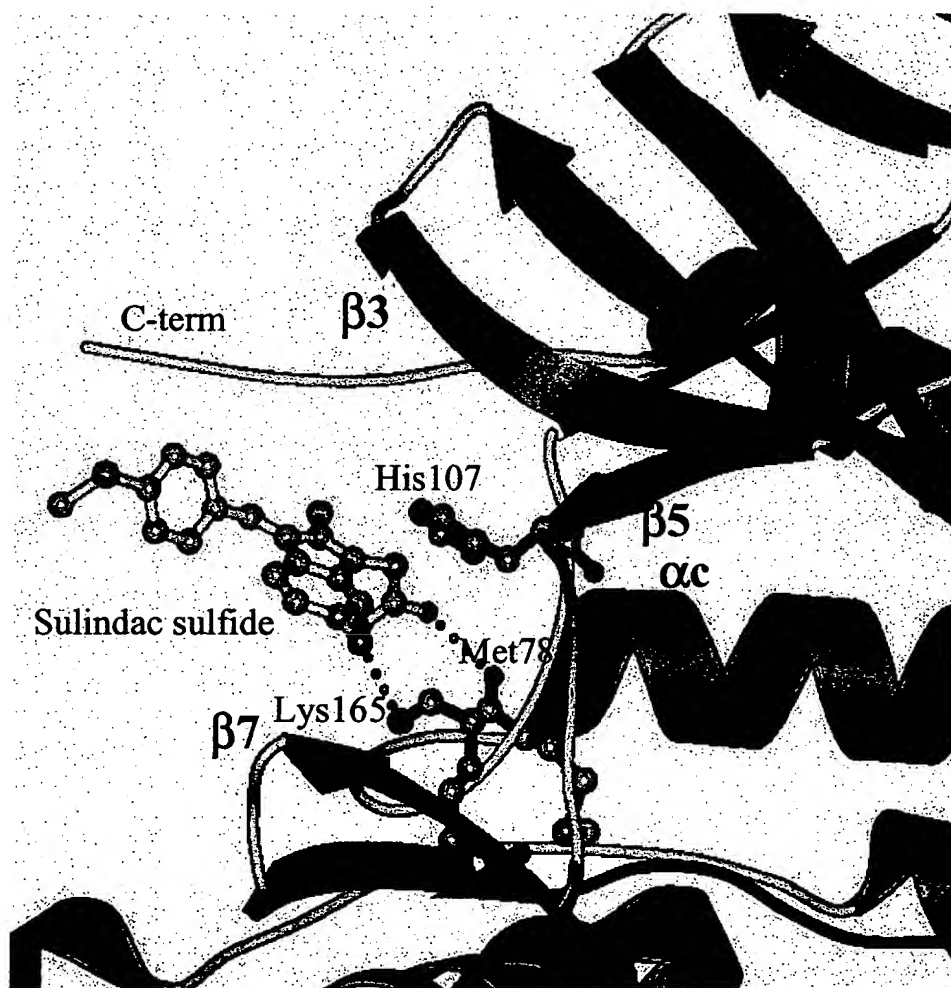


Fig. 3(a)

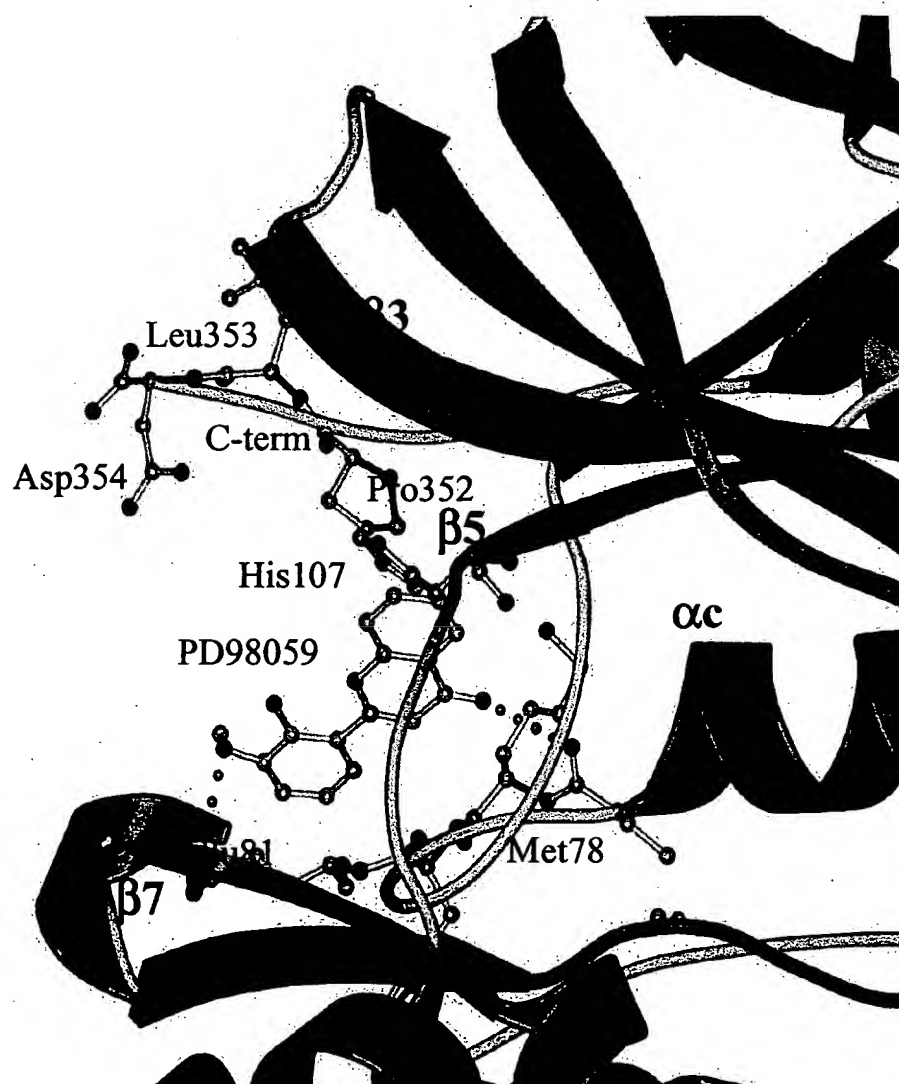


Fig. 3(b)

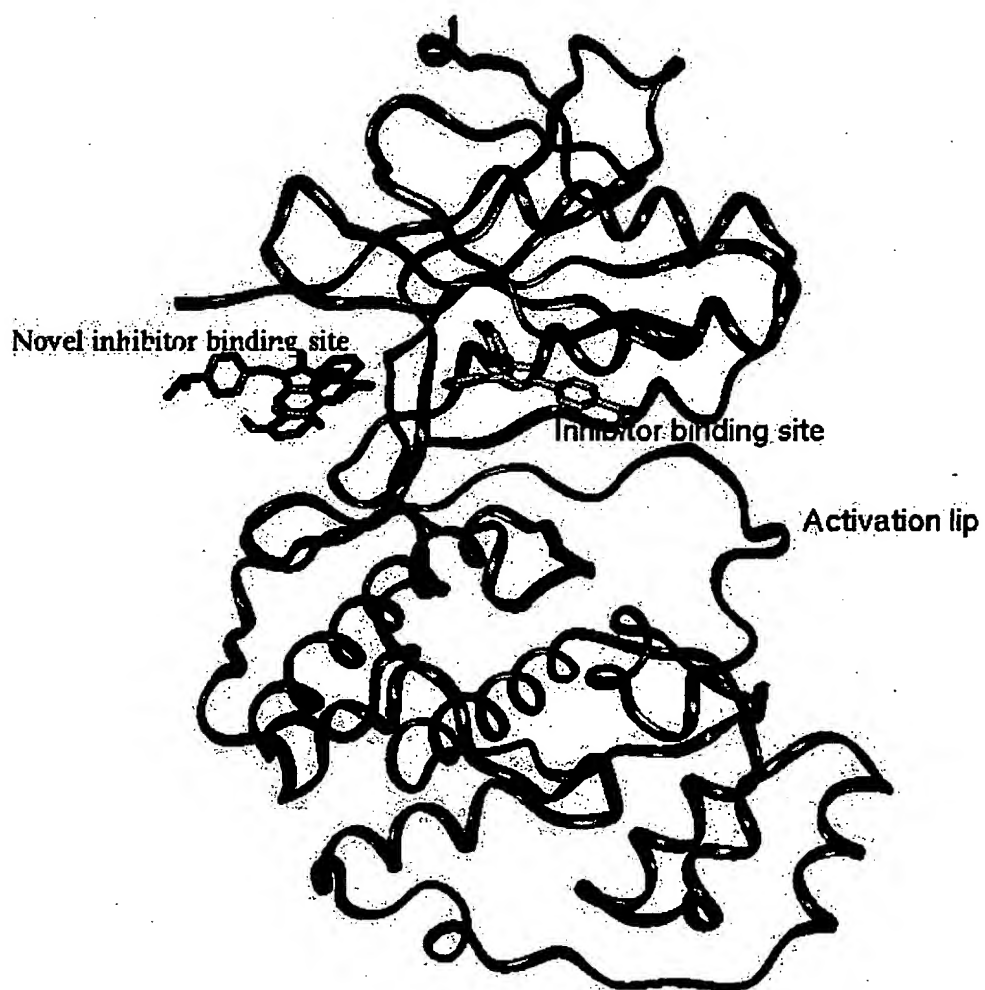


Fig. 4

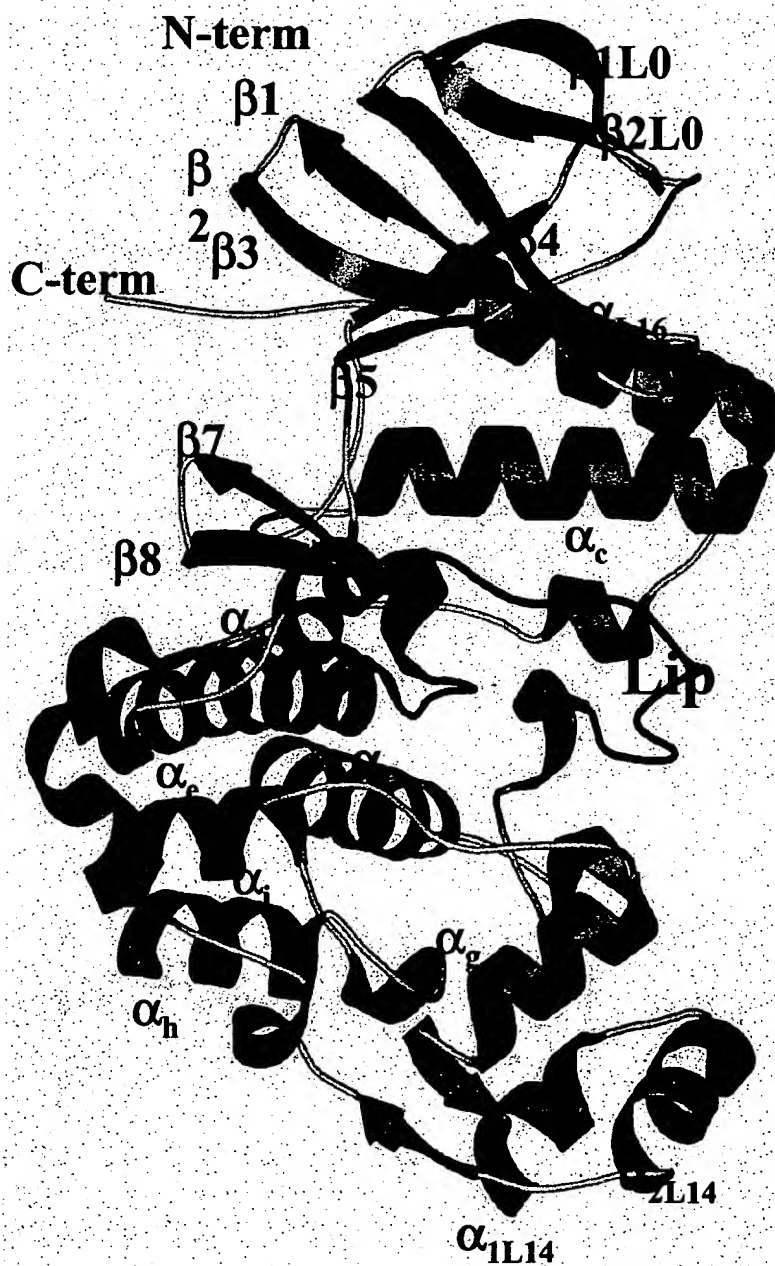


Fig. 5

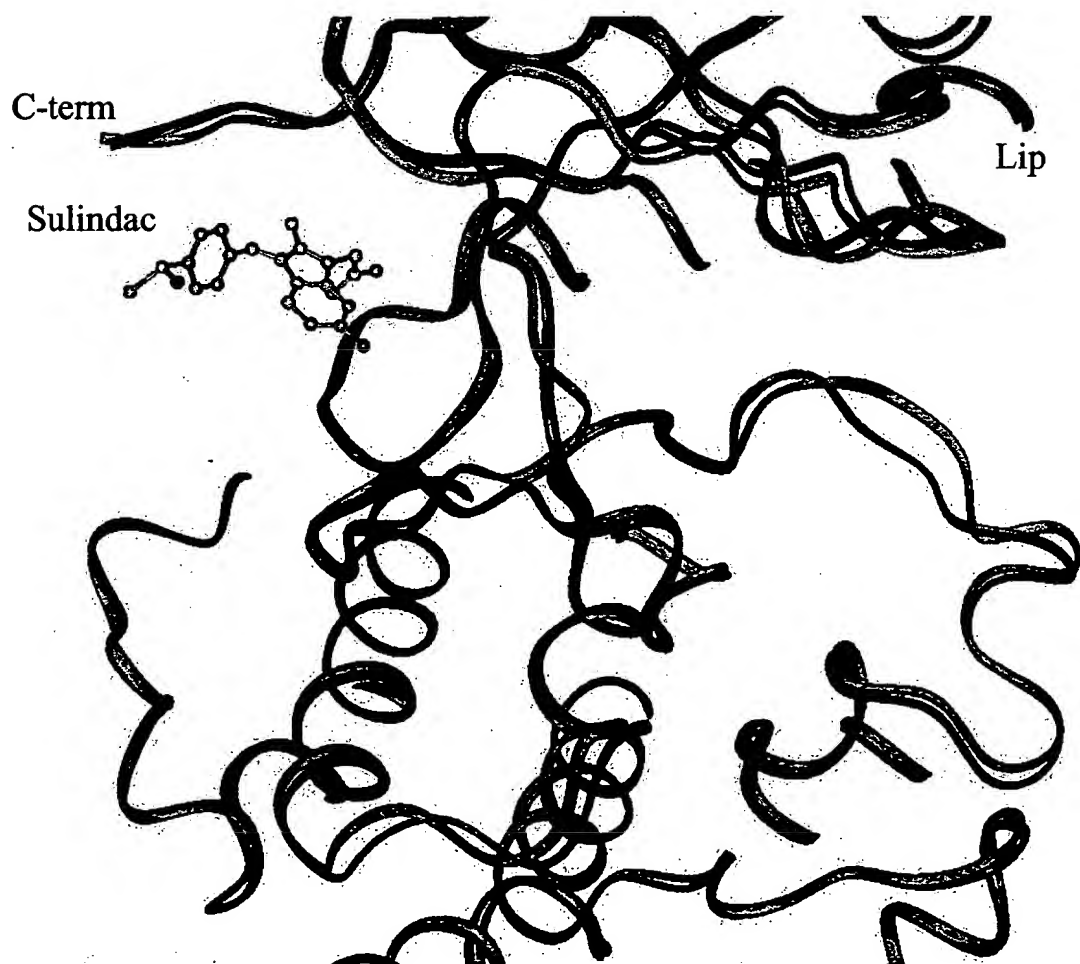


Fig. 6

Linker 2

P38	25	Q N L S - - - - - P V G S G A <u>Y</u> G S V C - - - - - A A F
IKK	21	- - - - - L G T G G <u>F</u> G N V I - - - - - R W H
MEK1	69	E K I S - - - - - E L G A G N G G V V F - - - - - K V S
JNK3	27	Q N L K - - - - - P I G S G A <u>Q</u> G I V C - - - - - A A Y
GSK3	52	Q E V S Y T D T K V I G N G S <u>F</u> G V V Y - - - - - Q A K
Akt	153	D Y L K - - - - - L L G K G T <u>F</u> G K V I - - - - - L V R
NIK	446	R D L T - - - - - E N V N G M A M N L T T Q V R E I A K V

Helix C

P38	63	I H A K R T Y R E L - - - - - R L <u>L</u> K H
IKK	53	K N R D R W C L E I - - - - - Q I M R R
MEK1	107	I R - N Q I I R E L - - - - - Q V <u>L</u> H E
JNK3	65	T H A K R A Y R E L - - - - - V L <u>M</u> K C
GSK3	91	- - K R F K N R E L - - - - - Q I <u>M</u> R K
Akt	192	D E V A H T V T E S - - - - - R V <u>L</u> Q N
NIK	491	L D L K N T I N T M V D R L G T F A F E V S K V

Linker 5

P38	78	M <u>K</u> H <u>E</u> N V I G
IKK	68	L N H <u>P</u> N V V A
MEK1	121	C <u>N</u> S <u>P</u> Y I V G
JNK3	80	V N H <u>K</u> N I I S
GSK3	104	L D H C N I V R
Akt	207	T R H <u>P</u> F L T A
NIK	515	A R E <u>V</u> G T D G

Crossover

P38	100	N - D V Y L V <u>T</u> <u>H</u> L M G A D L - - - - N - N
IKK	90	D L P L L A M E <u>Y</u> C Q G G D L R R Y L N - Q
MEK1	142	- - - - I C M E <u>H</u> M D G G S L - - - - D - Q
JNK3	102	Q - D V Y L V <u>M</u> <u>E</u> L M D A N L - - - - C - Q
GSK3	119	V - Y L N L V L <u>D</u> Y V P E T V - - - - Y - R
Akt	226	- - - C F V M E <u>Y</u> A N G G D L - - - - F F H
NIK	538	K - D L T E N V N T M A S N L - - - - T - S

C-Terminus

P38	345	V I S F V P P P L D Q E
IKK	359	L V L L P D K P A T Q C
MEK1	385	N Q P S T P T H A A S I
JNK3	363	V M N S E - - - - -
GSK3	374	A T I L I P P H A R I Q
Akt	464	L D Q R T H F P Q F S Y
NIK	788	V F N A L K T L A V K E

Fig. 7